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Estimating the Number of Discrete Models of Biological Networks

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Design of experiments and model selection are typically viewed as unrelated processes in the inference of biological networks. Recently we developed an algebraic framework to unify these two processes for discrete data and polynomials over a finite field. Input data are paired with monomial bases of polynomial models, thereby enabling the simultaneous execution of experimental design and model selection. An advantage of the framework is increased efficiency in network inference by providing a comprehensive view of all possible model bases associated to a data set. In this talk we highlight aspects of this work and give special attention to estimating the number of models associated to a data set.